GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2003, 03:03:40 ; Search time 227.079 Seconds
(without alignments)
797.438 Million cell updates/sec

Title: US-09-698-781-3
Perfect score: 1436
Sequence: 1 MKQILHPALETTAMTLFPVL.....KHQLVRDSCKASCNCSNSIY 258

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 501302 seqs, 350932545 residues

Total number of hits satisfying chosen parameters: 1002604

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09698781/runat_07032003_083459_5337/app_query.fasta_1.654
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09698781_@CGN_1_1_71_@runat_07032003_083459_5337
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1386	96.5	2128	9	US-10-099-570-1	Sequence 1, Appli
2	1386	96.5	2128	10	US-09-962-832-257	Sequence 257, App
3	337.5	23.5	1008	10	US-09-876-225-1	Sequence 1, Appli
4	318	22.1	3804	10	US-09-925-301-11	Sequence 11, Appl
5	314	21.9	441	10	US-09-960-352-2616	Sequence 2616, Ap
6	305.5	21.3	882	9	US-10-028-072-261	Sequence 261, App
7	305.5	21.3	882	9	US-10-121-049-261	Sequence 261, App
8	305.5	21.3	882	9	US-10-123-904-261	Sequence 261, App
9	305.5	21.3	882	9	US-10-140-470-261	Sequence 261, App
10	305.5	21.3	882	9	US-10-175-746-261	Sequence 261, App
11	305.5	21.3	882	9	US-10-176-918-261	Sequence 261, App
12	305.5	21.3	882	9	US-10-176-921-261	Sequence 261, App
13	305.5	21.3	882	9	US-10-137-865-261	Sequence 261, App
14	305.5	21.3	882	9	US-10-140-474-261	Sequence 261, App
15	305.5	21.3	882	9	US-10-142-431-261	Sequence 261, App
16	305.5	21.3	882	9	US-10-143-114-261	Sequence 261, App
17	305.5	21.3	882	9	US-10-140-002-261	Sequence 261, App
18	305.5	21.3	882	9	US-10-142-419-261	Sequence 261, App
19	296.5	20.6	1824	9	US-10-227-884-55	Sequence 55, Appl
20	296.5	20.6	1824	9	US-10-230-163-55	Sequence 55, Appl
21	296.5	20.6	1824	9	US-10-218-631-55	Sequence 55, Appl
22	296.5	20.6	1824	9	US-10-230-338-55	Sequence 55, Appl
c 23	296.5	20.6	4877	10	US-09-834-975-872	Sequence 872, App
c 24	296.5	20.6	4877	10	US-09-834-975-873	Sequence 873, App
c 25	296.5	20.6	4877	10	US-09-834-975-884	Sequence 884, App
26	291	20.3	1875	9	US-09-905-291A-284	Sequence 284, App
27	291	20.3	1875	9	US-09-902-853-284	Sequence 284, App
28	291	20.3	1875	9	US-09-907-824-284	Sequence 284, App
29	291	20.3	1875	9	US-09-907-841-284	Sequence 284, App
30	291	20.3	1875	9	US-09-904-011-284	Sequence 284, App
31	291	20.3	1875	9	US-10-028-072-359	Sequence 359, App
32	291	20.3	1875	9	US-09-906-742-284	Sequence 284, App
33	291	20.3	1875	9	US-10-121-049-359	Sequence 359, App
34	291	20.3	1875	9	US-10-123-904-359	Sequence 359, App
35	291	20.3	1875	9	US-10-140-470-359	Sequence 359, App
36	291	20.3	1875	9	US-09-906-838-284	Sequence 284, App
37	291	20.3	1875	9	US-09-907-613-284	Sequence 284, App
38	291	20.3	1875	9	US-09-907-942-284	Sequence 284, App
39	291	20.3	1875	9	US-10-175-746-359	Sequence 359, App
40	291	20.3	1875	9	US-10-176-918-359	Sequence 359, App
41	291	20.3	1875	9	US-10-176-921-359	Sequence 359, App
42	291	20.3	1875	9	US-10-137-865-359	Sequence 359, App
43	291	20.3	1875	9	US-10-140-474-359	Sequence 359, App
44	291	20.3	1875	9	US-09-904-820-284	Sequence 284, App
45	291	20.3	1875	9	US-09-904-859-284	Sequence 284, App

ALIGNMENTS

RESULT 1
US-10-099-570-1
; Sequence 1, Application US/10099570
; Publication No. US20030027178A1
; GENERAL INFORMATION:
; APPLICANT: Vasmatzis, George
; APPLICANT: Kosari, Farhad
; APPLICANT: Asmann, Yan
; APPLICANT: Cheville, John
; TITLE OF INVENTION: Methods and Kits for Determining a
; TITLE OF INVENTION: Cancer Diagnosis and Prognosis
; FILE REFERENCE: 07039-275001
; CURRENT APPLICATION NUMBER: US/10/099,570
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/276,523
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2128
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-099-570-1

Alignment Scores:
Pred. No.: 1.2e-152 Length: 2128
Score: 1386.00 Matches: 249
Percent Similarity: 99.60% Conservative: 0

```
Best Local Similarity:  99.60%          Mismatches:    1
Query Match:            96.52%          Indels:        0
DB:                     9               Gaps:          0

US-09-698-781-3 (1-258) x US-10-099-570-1 (1-2128)

Qy       9 LeuGluThrThrAlaMetThrLeuProValLeuLeuPheLeuValAlaGlyLeuLeu 28
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGGAAACCACTGCAATGACATTATTCCCAGTGCTGTTGTTCCTGGTTGCTGGGCTGCTT 60

Qy      29 ProSerPheProAlaAsnGluAspLysAspProAlaPheThrAlaLeuLeuThrThrGln 48
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCTTTTACTGCTTTGTTAACCACCCAA 120

Qy      49 ThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArgArgAlaValSerPro 68
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ACACAAGTGCAAAGGGAGATTGTGAATAAGCACAATGAACTGAGGAGAGCAGTATCTCCC 180

Qy      69 ProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAlaAlaAsnAlaGlnLys 88
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCTGCCAGAAACATGCTGAAGATGGAATGGAACAAAGAGGCTGCAGCAAATGCCCAAAAG 240

Qy      89 TrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArgMetThrSerLeuLys 108
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TGGGCAAACCAGTGCAATTACAGACACAGTAACCCAAAGGATCGAATGACAAGTCTAAAA 300

Qy     109 CysGlyGluAsnLeuTyrMetSerSerAlaProSerSerTrpSerGlnAlaIleGlnSer 128
           |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db     301 TGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAGCTCATGGTCACAAGCAATCCAAAGC 360

Qy     129 TrpPheAspGluTyrAsnAspPheAspPheGlyValGlyProLysThrProAsnAlaVal 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TGGTTTGATGAGTACAATGATTTTGACTTTGGTGTAGGGCCAAAGACTCCCAACGCAGTG 420

Qy     149 ValGlyHisTyrThrGlnValValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAla 168
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GTTGGACATTATACACAGGTTGTTTGGTACTCTTCATACCTCGTTGGATGTGGAAATGCC 480

Qy     169 TyrCysProAsnGlnLysValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGly 188
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TACTGTCCCAATCAAAAAGTTCTAAAATACTACTATGTTTGCCAATATTGTCCTGCTGGT 540

Qy     189 AsnTrpAlaAsnArgLeuTyrValProTyrGluGlnGlyAlaProCysAlaSerCysPro 208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AATTGGGCTAATAGACTATATGTCCCTTATGAACAAGGAGCACCTTGTGCCAGTTGCCCA 600

Qy     209 AspAsnCysAspAspGlyLeuCysThrAsnGlyCysLysTyrGluAspLeuTyrSerAsn 228
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GATAACTGTGACGATGGACTATGCACCAATGGTTGCAAGTACGAAGATCTCTATAGTAAC 660

Qy     229 CysLysSerLeuLysLeuThrLeuThrCysLysHisGlnLeuValArgAspSerCysLys 248
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGTAAAAGTTTGAAGCTCACATTAACCTGTAAACATCAGTTGGTCAGGGACAGTTGCAAG 720

Qy     249 AlaSerCysAsnCysSerAsnSerIleTyr 258
           |||||||||||||||||||||||||||||
Db     721 GCCTCCTGCAATTGTTCAAACAGCATTTAT 750

RESULT 2
US-09-962-832-257
; Sequence 257, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-74
;  CURRENT APPLICATION NUMBER: US/09/962,832
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,077
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,280
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 257
;   LENGTH: 2128
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-962-832-257

Alignment Scores:
Pred. No.:              1.2e-152        Length:        2128
Score:                  1386.00         Matches:       249
Percent Similarity:     99.60%          Conservative:  0
Best Local Similarity:  99.60%          Mismatches:    1
Query Match:            96.52%          Indels:        0
DB:                     10              Gaps:          0

US-09-698-781-3 (1-258) x US-09-962-832-257 (1-2128)

Qy       9 LeuGluThrThrAlaMetThrLeuProValLeuLeuPheLeuValAlaGlyLeuLeu 28
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGGAAACCACTGCAATGACATTATTCCCAGTGCTGTTGTTCCTGGTTGCTGGGCTGCTT 60

Qy      29 ProSerPheProAlaAsnGluAspLysAspProAlaPheThrAlaLeuLeuThrThrGln 48
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CCATCTTTTCCAGCAAATGAAGATAAGGATCCCGCTTTTACTGCTTTGTTAACCACCCAA 120

Qy      49 ThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArgArgAlaValSerPro 68
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ACACAAGTGCAAAGGGAGATTGTGAATAAGCACAATGAACTGAGGAGAGCAGTATCTCCC 180

Qy      69 ProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAlaAlaAsnAlaGlnLys 88
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCTGCCAGAAACATGCTGAAGATGGAATGGAACAAAGAGGCTGCAGCAAATGCCCAAAAG 240

Qy      89 TrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArgMetThrSerLeuLys 108
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TGGGCAAACCAGTGCAATTACAGACACAGTAACCCAAAGGATCGAATGACAAGTCTAAAA 300

Qy     109 CysGlyGluAsnLeuTyrMetSerSerAlaProSerSerTrpSerGlnAlaIleGlnSer 128
           |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db     301 TGTGGTGAGAATCTCTACATGTCAAGTGCCTCCAGCTCATGGTCACAAGCAATCCAAAGC 360

Qy     129 TrpPheAspGluTyrAsnAspPheAspPheGlyValGlyProLysThrProAsnAlaVal 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TGGTTTGATGAGTACAATGATTTTGACTTTGGTGTAGGGCCAAAGACTCCCAACGCAGTG 420

Qy     149 ValGlyHisTyrThrGlnValValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAla 168
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GTTGGACATTATACACAGGTTGTTTGGTACTCTTCATACCTCGTTGGATGTGGAAATGCC 480

Qy     169 TyrCysProAsnGlnLysValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGly 188
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TACTGTCCCAATCAAAAAGTTCTAAAATACTACTATGTTTGCCAATATTGTCCTGCTGGT 540

Qy     189 AsnTrpAlaAsnArgLeuTyrValProTyrGluGlnGlyAlaProCysAlaSerCysPro 208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AATTGGGCTAATAGACTATATGTCCCTTATGAACAAGGAGCACCTTGTGCCAGTTGCCCA 600

Qy     209 AspAsnCysAspAspGlyLeuCysThrAsnGlyCysLysTyrGluAspLeuTyrSerAsn 228
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GATAACTGTGACGATGGACTATGCACCAATGGTTGCAAGTACGAAGATCTCTATAGTAAC 660

Qy     229 CysLysSerLeuLysLeuThrLeuThrCysLysHisGlnLeuValArgAspSerCysLys 248
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGTAAAAGTTTGAAGCTCACATTAACCTGTAAACATCAGTTGGTCAGGGACAGTTGCAAG 720

Qy     249 AlaSerCysAsnCysSerAsnSerIleTyr 258
           |||||||||||||||||||||||||||||
Db     721 GCCTCCTGCAATTGTTCAAACAGCATTTAT 750

RESULT 3
US-09-876-225-1
; Sequence 1, Application US/09876225
```

```
; Patent No. US20020052025A1
; GENERAL INFORMATION:
;  APPLICANT: Baylor College of Medicine
;  APPLICANT:  Thompson, Timothy C.
;  APPLICANT:  Ren, Chengzhen
;  TITLE OF INVENTION: RTVP Based Compositions and Methods for the Treatment of Prostate
;  FILE REFERENCE: 38594.0027
;  CURRENT APPLICATION NUMBER: US/09/876,225
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 60/209,989
;  PRIOR FILING DATE: 2000-06-08
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1008
;   TYPE: DNA
;   ORGANISM: Mus sp.
US-09-876-225-1

Alignment Scores:
Pred. No.:                3.75e-30        Length:          1008
Score:                    337.50          Matches:         92
Percent Similarity:       45.36%          Conservative:    35
Best Local Similarity:    32.86%          Mismatches:      88
Query Match:              23.50%          Indels:          65
DB:                       10              Gaps:            13

US-09-698-781-3 (1-258) x US-09-876-225-1 (1-1008)

Qy       4 IleLeuHisProAlaLeuGluThrThrAlaMetThrLeuPheProValLeuLeuPheLeu 23
           ||||||   ||||||         |||      |||:::      :::|||      :::
Db     122 ATTCTAGGTCCAGCA------GCAACCAGAGAGACCATGCAGGTCATCCTTGCTGTGATA 175

Qy      24 ValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAlaPheThrAla 43
           |||              :::   |||:::                  :::||||||||||
Db     176 GTC-----------------TGGATGGCTTCGTCTGTGTCTAGTTCTTCATTTACAGCA 217

Qy      44 LeuLeu---------ThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
                          |||                :::|||   |||      ||||||
Db     218 AGCACTTTGCCAGATATAACAAACGAGGACTTCATTAAAGAATGTGTTCAAGTTCACAAC 277

Qy      61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
           :::||||||      ||||||||||||||||||||||||||||   |||   |||:::
Db     278 CAGCTTCGGTCAAAAGTGAGTCCACCAGCCCGGAATATGCTGTACATGTCTTGGGACCCA 337

Qy      81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
           :::   |||      |||:::   |||          |||   :::::|||   ||||||
Db     338 AAACTAGCCCAAATTGCAAAAGCATGGACAAAATCTTGTGAATTTAAACAC---AACCCA 394

Qy     101 Lys-----------------AspArgMetThrSerLeuLysCysGlyGluAsnLeuTyr 114
           :::                          |||:::|||      |||||||||:::::::
Db     395 CAGCTGCATTCACGGATACACCCAAATTTCACCGCCCTG------GGAGAGAATATCTGG 448

Qy     115 MetSerSer---AlaProSerSerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyr 133
           :::   |||   :::      |||   |||   ||||||   :::|||:::::|||
Db     449 CTTGGCTCTCTATCCATCTTTTCAGTATCCTCAGCCATCTCTGCCTGGTATGAAGAAATT 508

Qy     134 AsnAspPheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThr 153
                :::|||||||           :::              |||   ||||||||||||
Db     509 AAGCACTATGACTTCAGCACT------AGGAAATGTAGACATGTCTGTGGCCATTATACT 562

Qy     154 GlnValValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGln 173
           ||||||||||||      ||||||   :::||||||                |||||||||
Db     563 CAGGTTGTTTGGGCAGACAGTTACAAACTTGGCTGTGCAGTGCAACTTTGCCCTAATGGA 622

Qy     174 LysValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArg 193
                          :::::|||   |||   ||||||||||||:::
Db     623 GCA------------AATTTTATATGCGACTATGGACCAGCAGGAAATTACCCAACG--- 667

Qy     194 LeuTyrValProTyrGluGlnGlyAlaProCysAlaSerCysProAspAsnCysAspAsp 213
                  ||||||:::||||||||||   |||:::   ||||||          |||
Db     668 ------TGGCCATATAAGCAAGGAGCCACGTGCAGTGATTGCCCA---------AAAGAT 712

Qy     214 GlyLeuCysThrAsnGlyCys------------------------------------ 220
                 |||   |||
Db     713 GACAAGTGTCTCAACAGTCTCTGATTAACCCACGACGAGACCAGGTCTCACGTTACTACT 772

Qy     221 -------------------------------------LysTyrGluAspLeuTyrSer 227
                                                   :::|||      |||:::
Db     773 CTGTCGCATTATCCAGACTGGCCTATATACCTGCGTAACAGATACACATCTCTCTTTCTC 832

Qy     228 AsnCysLysSerLeuLysLeu-----------------ThrLeuThrCysLysHisGln 241
                 |||||||:::  |||                 |||:::      |||||||:::
Db     833 ATTGCTAAGTCGGTTCTCCTATTACTGTCTGTTATAATTACCATCTGGGTAAAGCACAAA 892

RESULT 4
US-09-925-301-11
; Sequence 11, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA106
;  CURRENT APPLICATION NUMBER: US/09/925,301
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05882
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1694
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 3804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-301-11

Alignment Scores:
Pred. No.:                5.54e-27        Length:          3804
Score:                    318.00          Matches:         83
Percent Similarity:       48.51%          Conservative:    31
Best Local Similarity:    35.32%          Mismatches:      79
Query Match:              22.14%          Indels:          42
DB:                       10              Gaps:            12

US-09-698-781-3 (1-258) x US-09-925-301-11 (1-3804)

Qy       2 LysGlnIleLeuHisProAlaLeuGluThrThrAla---MetThrLeuPheProValLeu 20
           :::|||   :::          |||   |||   |||   |||      |||
Db     125 AGACAAAGCATGCGTGTCACACTTGCTACAATAGCCTGGATGGTTTCTTTTGTCTCCAAT 184

Qy      21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
                  |||  :::||||||             |||||||||
Db     185 TATTCACACACAGCAAATATTTTGCCAGATATC---GAAAATGAAGAT------------ 229

Qy      41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
                                                 ::::::   |||      ||||||
Db     230 ----------------------------TTCATCAAAGACTGCGTTCGAATCCATAAC 259

Qy      61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
           :::   |||      |||   |||   |||   :::||||||   |||   |||:::
Db     260 AAGTTCCGATCAGAGGTGAAACCAACAGCCAGTGATATGCTATACATGACTTGGGACCCA 319

Qy      81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSer------ 98
                 |||      |||:::   ||||||:::   |||   :::   |||:::
Db     320 GCACTAGCCCAAATTGCAAAAGCATGGGCCAGCAATTGCCAGTTTTCACATAATACACGG 379

Qy      99 ---AsnProLysAspArgMet-----------ThrSerLeuLysCysGlyGluAsnLeu 113
                 |||      ::::::           |||||||||      ||||||||||:::
Db     380 CTGAAGCCACCCCACAAGCTGCACCCAAACTTCACTTCACTG------GGAGAGAACATC 433

Qy     114 TyrMetSerSerAlaPro---SerSerTrpSerGlnAlaIleGlnSerTrpPheAspGlu 132
           :::      |||   |||      |||   |||   ||||||   :::|||:::||||||
Db     434 TGGACTGGGTCTGTGCCCATTTTTTCTGTGTCTTCCGCCATCACAAACTGGTATGACGAA 493

Qy     133 TyrAsnAspPheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyr 152
```

```
              |||:::||||||            :::            |||   |||||||||
Db    494 ATCCAGGACTATGACTTCAAGACT------CGGATATGCAAAAAAGTCTGTGGCCACTAC 547

Qy    153 ThrGlnValValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn 172
          ||||||||||||||      ||||||   |||||||||          :::|||||||
Db    548 ACTCAGGTTGTTTGGGCAGATAGTTACAAAGTTGGCTGCGCAGTTCAATTTTGCCCT--- 604

Qy    173 GlnLysValLeuLysTyr--------------------TyrTyrValCysGlnTyrCys 185
             ||||||      :::                   ::::::::|||   |||
Db    605 ---AAAGTTTCTGGCTTTGACGCTCTTTCCAATGGAGCACATTTTATATGCAACTACGGA 661

Qy    186 ProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGlnGlyAlaProCysAla 205
          |||   ||||||:::                  ||||||::::::||||||      :::
Db    662 CCAGGAGGGAATTACCCAACT---------TGGCCATATAAGAGAGGAGCCACCTKCAGT 712

Qy    206 SerCysProAspAsn------CysAspAspGlyLeuCysThrAsn 218
          :::|||||||:::|||      |||   |||   ||||||   |||
Db    713 GCCTGCCCCAATAATGACAAGTGTTTGGACAATCTCTGTGTTAAC 757

RESULT 5
US-09-960-352-2616
; Sequence 2616, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2616
;   LENGTH: 441
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 12-LIB2809-005-Q1-E1-C7
US-09-960-352-2616

Alignment Scores:
Pred. No.:              6.05e-28      Length:          441
Score:                  314.00        Matches:         50
Percent Similarity:     75.95%        Conservative:    10
Best Local Similarity:  63.29%        Mismatches:      19
Query Match:            21.87%        Indels:          0
DB:                     10            Gaps:            0

US-09-698-781-3 (1-258) x US-09-960-352-2616 (1-441)

Qy    180 TyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGlu 199
          |||||||||||||||||||||||||||||         |||   :::|||||||||:::
Db      6 TATGTATGCCAATACTGTCCTGCTGGTAATATTGTTGGCAGACAACATGTCCCTTACCAA 65

Qy    200 GlnGlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGly 219
          :::|||   ||||||   ||||||||||::::::|||||||:::|||||||||||||||
Db     66 AAGGGAACACCTTGTGGCAGCTGCCCCAATCATTGTGACAACGGACTATGCACCAATAGT 125

Qy    220 CysLysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLys 239
          |||:::||||||||||   ||||||||||||   |||||||||   |||   ||||||
Db    126 TGTGAGTATGAAGATACCTATTCTAACTGTGCATCTTTAAAGGAAACATGGACCTGTGCC 185

Qy    240 HisGlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
                |||:::   :::||||||||||:::||||||||         ||||||
Db    186 TCTGATTTTGTGAAGACCAATTGCAAGGCTGCCTGCAATTGTCAAGGCAAAATTTAT 242

RESULT 6
US-10-028-072-261
; Sequence 261, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang
;  TITLE OF INVENTION:
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/028,072
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059836
;  PRIOR FILING DATE: 1997-09-24
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/062285
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/062287
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/062814
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/062816
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063045
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063082
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/063127
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063327
;  PRIOR FILING DATE: 1997-10-27
;  PRIOR APPLICATION NUMBER: 60/063329
;  PRIOR FILING DATE: 1997-10-27
;  PRIOR APPLICATION NUMBER: 60/063550
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063561
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063704
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063733
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063735
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 60/063738
```

; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064248
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/064809
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065846
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066453
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069212
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069278
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069334
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069694
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 60/072320
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081695
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081818
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086414
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086430
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 19/98-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Alignment Scores:

Pred. No.:	1.74e-26	Length:	882
Score:	305.50	Matches:	80
Percent Similarity:	49.55%	Conservative:	31
Best Local Similarity:	35.71%	Mismatches:	82
Query Match:	21.27%	Indels:	31
DB:	9	Gaps:	10

US-09-698-781-3 (1-258) x US-10-028-072-261 (1-882)

```
Qy       6 HisPro------AlaLeuGluThrThrAlaMetThrLeuProValLeuLeuPheLeu 23
           ||||||      ||||||:::               |||:::   :::   |||   |||
Db      82 CATCCTTCCATGGCTCTGAAGAATAAATTCAGTTGTTTATGGATCTTGGGTCTGTGTTTG 141

Qy      24 ValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAlaPheThrAla 43
           ||||||                 |||:::           ||||||   |||
Db     142 GTAGCCACTACATCTTCCAAAATCCCATCC------ATCACTGACCCACACTTTATA--- 192

Qy      44 LeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArg 63
                                          :::      |||||||||   |||
Db     193 -------------------------GACAACTGCATAGAAGCCCACAACGAATGGCGT 225
```

```
Qy      64 ArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAla 83
           |||:::|||||||||   :::|||      |||   |||:::|||      |||
Db     226 GGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACATGATTTGGGATAAAGGTTTAGCA 285

Qy      84 AlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArg 103
           |||:::   ||||||||||||||   :::   |||::::::      |||:::
Db     286 AAGATGGCTAAAGCATGGGCAAACCAGTGCAAATTTGAACATAATGACTGTTTGGATAAA 345

Qy     104 MetThrSerLeuLysCys--------------------GlyGluAsnLeuTyrMetSer 116
           |||   ||||||                         |||||||||:::::::::
Db     346 ------TCATATAAATGCTATGCAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGT 399

Qy     117 SerAlaProSer---SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAsp 135
               |||   :::         ||||||   :::|||::::::|||
Db     400 GGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGGTATAATGAAACCCAATTT 459

Qy     136 PheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnVal 155
           :::||||||                :::   :::   |||   |||||||||||||||:::
Db     460 TATGATTTT------GATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACAGTTA 513

Qy     156 ValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn---GlnLys 174
           ||||||   :::|||:::   |||||||||      |||   |||||||||
Db     514 GTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTTGGGGGA 573

Qy     175 ValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeu 194
                  :::|||||||   |||   |||||||||||||:::||||||
Db     574 GCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAAT------ 627

Qy     195 TyrValProTyrGluGlnGlyAlaProCysAlaSerCys------ProAspAsnCysAsp 212
           ||||||   :::|||      |||:::   |||         :::   |||
Db     628 ATGCCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTA 687

Qy     213 AspGlyLeuCys 216
           ||||||
Db     688 AAGAACCTCTGC 699

RESULT 7
US-10-121-049-261
; Sequence 261, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C17
;  CURRENT APPLICATION NUMBER: US/10/121,049
;  CURRENT FILING DATE:  2002-04-12
;       Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 261
;   LENGTH: 882
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-121-049-261

Alignment Scores:
Pred. No.:              1.74e-26        Length:         882
Score:                  305.50          Matches:        80
Percent Similarity:     49.55%          Conservative:   31
Best Local Similarity:  35.71%          Mismatches:     82
Query Match:            21.27%          Indels:         31
DB:                     9               Gaps:           10

US-09-698-781-3 (1-258) x US-10-121-049-261 (1-882)

Qy       6 HisPro------AlaLeuGluThrThrAlaMetThrLeuProValLeuLeuPheLeu 23
           ||||||      |||||||:::                |||:::   :::   |||   |||
Db      82 CATCCTTCCATGGCTCTGAAGAATAAATTCAGTTGTTTATGGATCTTGGGTCTGTGTTTG 141

Qy      24 ValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAlaPheThrAla 43
           ||||||                  |||:::              ||||||   |||
Db     142 GTAGCCACTACATCTTCCAAAATCCCATCC------ATCACTGACCCACACTTTATA--- 192

Qy      44 LeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArg 63
                                                :::      |||||||||   |||
Db     193 --------------------------GACAACTGCATAGAAGCCCACAACGAATGGCGT 225

Qy      64 ArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAla 83
           |||:::|||||||||   :::|||      |||   |||:::|||      |||
Db     226 GGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACATGATTTGGGATAAAGGTTTAGCA 285

Qy      84 AlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArg 103
           |||:::   ||||||||||||||   :::   |||::::::      |||:::
Db     286 AAGATGGCTAAAGCATGGGCAAACCAGTGCAAATTTGAACATAATGACTGTTTGGATAAA 345

Qy     104 MetThrSerLeuLysCys--------------------GlyGluAsnLeuTyrMetSer 116
           |||   ||||||                         |||||||||:::::::::
Db     346 ------TCATATAAATGCTATGCAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGT 399

Qy     117 SerAlaProSer---SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAsp 135
               |||   :::         ||||||   :::|||::::::|||
Db     400 GGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGGTATAATGAAACCCAATTT 459

Qy     136 PheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnVal 155
           :::||||||                :::   :::   |||   |||||||||||||||:::
Db     460 TATGATTTT------GATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACAGTTA 513

Qy     156 ValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn---GlnLys 174
           ||||||   :::|||:::   |||||||||      |||   |||||||||
Db     514 GTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTTGGGGGA 573

Qy     175 ValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeu 194
                  :::|||||||   |||   |||||||||||||:::||||||
Db     574 GCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAAT------ 627

Qy     195 TyrValProTyrGluGlnGlyAlaProCysAlaSerCys------ProAspAsnCysAsp 212
           ||||||   :::|||      |||:::   |||         :::   |||
Db     628 ATGCCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTA 687

Qy     213 AspGlyLeuCys 216
           ||||||
Db     688 AAGAACCTCTGC 699

RESULT 8
US-10-123-904-261
; Sequence 261, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
```

```
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C54
;  CURRENT APPLICATION NUMBER: US/10/123,904
;  CURRENT FILING DATE:  2002-04-16
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 261
;   LENGTH: 882
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-123-904-261

Alignment Scores:
Pred. No.:              1.74e-26      Length:          882
Score:                  305.50        Matches:         80
Percent Similarity:     49.55%        Conservative:    31
Best Local Similarity:  35.71%        Mismatches:      82
Query Match:            21.27%        Indels:          31
DB:                     9             Gaps:            10

US-09-698-781-3 (1-258) x US-10-123-904-261 (1-882)

Qy      6 HisPro------AlaLeuGluThrThrAlaMetThrLeuPheProValLeuLeuPheLeu 23
          ||||||      |||||||:::                 |||:::   :::   |||   |||
Db     82 CATCCTTCCATGGCTCTGAAGAATAAATTCAGTTGTTTATGGATCTTGGGTCTGTGTTTG 141

Qy     24 ValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAlaPheThrAla 43
          ||||||                  |||:::           ||||||   |||
Db    142 GTAGCCACTACATCTTCCAAAATCCCATCC------ATCACTGACCCACACTTTATA--- 192

Qy     44 LeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArg 63
                                        :::      |||||||||   |||
Db    193 --------------------------GACAACTGCATAGAAGCCCACAACGAATGGCGT 225

Qy     64 ArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAla 83
             |||:::|||||||||   :::|||      |||   |||:::|||      |||
Db    226 GGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACATGATTTGGGATAAAGGTTTAGCA 285

Qy     84 AlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArg 103
             |||:::   ||||||||||||||   :::   |||::::::      |||:::
Db    286 AAGATGGCTAAAGCATGGGCAAACCAGTGCAAATTTGAACATAATGACTGTTTGGATAAA 345

Qy    104 MetThrSerLeuLysCys--------------------GlyGluAsnLeuTyrMetSer 116
             |||   ||||||                       |||||||||:::::::::
Db    346 ------TCATATAAATGCTATGCAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGT 399

Qy    117 SerAlaProSer---SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAsp 135
                |||   :::         ||||||   :::|||:::::::|||
Db    400 GGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGGTATAATGAAACCCAATTT 459

Qy    136 PheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnVal 155
          :::||||||                 :::   :::   |||   |||||||||||||||:::
Db    460 TATGATTTT------GATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACAGTTA 513

Qy    156 ValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn---GlnLys 174
          ||||||   :::|||:::   |||||||||      |||   |||||||||
Db    514 GTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTTGGGGGA 573

Qy    175 ValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeu 194
                    :::||||||   |||   ||||||||||||||:::||||||
Db    574 GCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAAT------ 627

Qy    195 TyrValProTyrGluGlnGlyAlaProCysAlaSerCys------ProAspAsnCysAsp 212
          ||||||   :::|||      |||:::   |||         :::   |||
Db    628 ATGCCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTA 687

Qy    213 AspGlyLeuCys 216
```

```
                ||||||
Db    688 AAGAACCTCTGC 699

RESULT 9
US-10-140-470-261
; Sequence 261, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C160
;  CURRENT APPLICATION NUMBER: US/10/140,470
;  CURRENT FILING DATE:  2002-05-06
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 261
;   LENGTH: 882
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-140-470-261

Alignment Scores:
Pred. No.:              1.74e-26      Length:          882
Score:                  305.50        Matches:         80
Percent Similarity:     49.55%        Conservative:    31
Best Local Similarity:  35.71%        Mismatches:      82
Query Match:            21.27%        Indels:          31
DB:                     9             Gaps:            10

US-09-698-781-3 (1-258) x US-10-140-470-261 (1-882)

Qy      6 HisPro------AlaLeuGluThrThrAlaMetThrLeuPheProValLeuLeuPheLeu 23
          ||||||      |||||||:::                 |||:::   :::   |||   |||
Db     82 CATCCTTCCATGGCTCTGAAGAATAAATTCAGTTGTTTATGGATCTTGGGTCTGTGTTTG 141

Qy     24 ValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAlaPheThrAla 43
          ||||||                  |||:::           ||||||   |||
Db    142 GTAGCCACTACATCTTCCAAAATCCCATCC------ATCACTGACCCACACTTTATA--- 192

Qy     44 LeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArg 63
                                        :::      |||||||||   |||
Db    193 --------------------------GACAACTGCATAGAAGCCCACAACGAATGGCGT 225

Qy     64 ArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAla 83
             |||:::|||||||||   :::|||      |||   |||:::|||      |||
Db    226 GGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACATGATTTGGGATAAAGGTTTAGCA 285

Qy     84 AlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArg 103
             |||:::   ||||||||||||||   :::   |||::::::      |||:::
Db    286 AAGATGGCTAAAGCATGGGCAAACCAGTGCAAATTTGAACATAATGACTGTTTGGATAAA 345

Qy    104 MetThrSerLeuLysCys--------------------GlyGluAsnLeuTyrMetSer 116
             |||   ||||||                       |||||||||:::::::::
Db    346 ------TCATATAAATGCTATGCAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGT 399

Qy    117 SerAlaProSer---SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAsp 135
```

```
                  |||   :::         ||||||   :::|||:::::::|||
Db    400 GGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGGTATAATGAAACCCAATTT 459

Qy    136 PheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnVal 155
          :::||||||             :::   :::   |||   ||||||||||||||||:::
Db    460 TATGATTTT------GATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACAGTTA 513

Qy    156 ValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn---GlnLys 174
          ||||||   :::|||:::   |||||||||       |||   |||||||||
Db    514 GTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTTGGGGGA 573

Qy    175 ValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeu 194
                  :::||||||   |||   ||||||||||||:::||||||
Db    574 GCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAAT------ 627

Qy    195 TyrValProTyrGluGlnGlyAlaProCysAlaSerCys------ProAspAsnCysAsp 212
          ||||||   :::|||       |||:::   |||          :::   |||
Db    628 ATGCCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTA 687

Qy    213 AspGlyLeuCys 216
          ||||||
Db    688 AAGAACCTCTGC 699

RESULT 10
US-10-175-746-261
; Sequence 261, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C353
;  CURRENT APPLICATION NUMBER: US/10/175,746
;  CURRENT FILING DATE:  2002-06-19
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 261
;   LENGTH: 882
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-175-746-261

Alignment Scores:
Pred. No.:              1.74e-26        Length:         882
Score:                  305.50          Matches:        80
Percent Similarity:     49.55%          Conservative:   31
Best Local Similarity:  35.71%          Mismatches:     82
Query Match:            21.27%          Indels:         31
DB:                     9               Gaps:           10

US-09-698-781-3 (1-258) x US-10-175-746-261 (1-882)

Qy      6 HisPro------AlaLeuGluThrThrAlaMetThrLeuProValLeuLeuPheLeu 23
          ||||||      |||||||:::               |||:::   :::   |||   |||
Db     82 CATCCTTCCATGGCTCTGAAGAATAAATTCAGTTGTTTATGGATCTTGGGTCTGTGTTTG 141

Qy     24 ValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAlaPheThrAla 43
          ||||||                  |||:::           ||||||   |||
Db    142 GTAGCCACTACATCTTCCAAAATCCCATCC------ATCACTGACCCACACTTTATA--- 192

Qy     44 LeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArg 63
                                                 :::      |||||||||   |||
Db    193 --------------------------GACAACTGCATAGAAGCCCACAACGAATGGCGT 225

Qy     64 ArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAla 83
          |||:::|||||||||   :::|||      |||   |||:::|||      |||
Db    226 GGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACATGATTTGGGATAAAGGTTTAGCA 285

Qy     84 AlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArg 103
          |||:::  ||||||||||||||   :::   |||::::::      |||:::
Db    286 AAGATGGCTAAAGCATGGGCAAACCAGTGCAAATTTGAACATAATGACTGTTTGGATAAA 345

Qy    104 MetThrSerLeuLysCys--------------------GlyGluAsnLeuTyrMetSer 116
          |||   ||||||                         |||||||||:::::::::
Db    346 ------TCATATAAATGCTATGCAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGT 399

Qy    117 SerAlaProSer---SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAsp 135
                |||   :::         ||||||   :::|||:::::::|||
Db    400 GGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGGTATAATGAAACCCAATTT 459

Qy    136 PheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnVal 155
          :::||||||             :::   :::   |||   ||||||||||||||||:::
Db    460 TATGATTTT------GATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACAGTTA 513

Qy    156 ValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn---GlnLys 174
          ||||||   :::|||:::   |||||||||       |||   |||||||||
Db    514 GTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTTGGGGGA 573

Qy    175 ValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeu 194
                  :::||||||   |||   ||||||||||||:::||||||
Db    574 GCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAAT------ 627

Qy    195 TyrValProTyrGluGlnGlyAlaProCysAlaSerCys------ProAspAsnCysAsp 212
          ||||||   :::|||       |||:::   |||          :::   |||
Db    628 ATGCCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTA 687

Qy    213 AspGlyLeuCys 216
          ||||||
Db    688 AAGAACCTCTGC 699

RESULT 11
US-10-176-918-261
; Sequence 261, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C382
;  CURRENT APPLICATION NUMBER: US/10/176,918
;  CURRENT FILING DATE:  2002-06-20
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 261
```

```
;   LENGTH: 882
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-176-918-261

Alignment Scores:
Pred. No.:              1.74e-26        Length:         882
Score:                  305.50          Matches:        80
Percent Similarity:     49.55%          Conservative:   31
Best Local Similarity:  35.71%          Mismatches:     82
Query Match:            21.27%          Indels:         31
DB:                     9               Gaps:           10

US-09-698-781-3 (1-258) x US-10-176-918-261 (1-882)

Qy       6 HisPro------AlaLeuGluThrThrAlaMetThrLeuPheProValLeuLeuPheLeu 23
           ||||||      |||||||:::           |||:::   :::   |||   |||
Db      82 CATCCTTCCATGGCTCTGAAGAATAAATTCAGTTGTTTATGGATCTTGGGTCTGTGTTTG 141

Qy      24 ValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAlaPheThrAla 43
           ||||||                |||:::          ||||||   |||
Db     142 GTAGCCACTACATCTTCCAAAATCCCATCC------ATCACTGACCCACACTTTATA--- 192

Qy      44 LeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArg 63
                                          :::      |||||||||   |||
Db     193 --------------------------GACAACTGCATAGAAGCCCACAACGAATGGCGT 225

Qy      64 ArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAla 83
             |||:::|||||||||  :::|||      |||   |||:::|||      |||
Db     226 GGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACATGATTTGGGATAAAGGTTTAGCA 285

Qy      84 AlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArg 103
             |||:::   ||||||||||||||   :::   |||::::::      |||:::
Db     286 AAGATGGCTAAAGCATGGGCAAACCAGTGCAAATTTGAACATAATGACTGTTTGGATAAA 345

Qy     104 MetThrSerLeuLysCys--------------------GlyGluAsnLeuTyrMetSer 116
             |||   ||||||                        |||||||||:::::::::
Db     346 ------TCATATAAATGCTATGCAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGT 399

Qy     117 SerAlaProSer---SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAsp 135
                 |||   :::        ||||||   :::|||:::::|||
Db     400 GGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGGTATAATGAAACCCAATTT 459

Qy     136 PheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnVal 155
           :::||||||                :::   :::   |||   |||||||||||||||:::
Db     460 TATGATTTT------GATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACAGTTA 513

Qy     156 ValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn---GlnLys 174
           ||||||   :::|||:::   |||||||||      |||   |||||||||
Db     514 GTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTTGGGGGA 573

Qy     175 ValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeu 194
                    :::||||||   |||   ||||||||||||:::||||||
Db     574 GCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAAT------ 627

Qy     195 TyrValProTyrGluGlnGlyAlaProCysAlaSerCys------ProAspAsnCysAsp 212
             ||||||   :::|||      |||:::   |||          :::   |||
Db     628 ATGCCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTA 687

Qy     213 AspGlyLeuCys 216
             ||||||.
Db     688 AAGAACCTCTGC 699

RESULT 12
US-10-176-921-261
; Sequence 261, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C288
;  CURRENT APPLICATION NUMBER: US/10/176,921
;  CURRENT FILING DATE:  2002-06-20
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 261
;   LENGTH: 882
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-176-921-261

Alignment Scores:
Pred. No.:              1.74e-26        Length:         882
Score:                  305.50          Matches:        80
Percent Similarity:     49.55%          Conservative:   31
Best Local Similarity:  35.71%          Mismatches:     82
Query Match:            21.27%          Indels:         31
DB:                     9               Gaps:           10

US-09-698-781-3 (1-258) x US-10-176-921-261 (1-882)

Qy       6 HisPro------AlaLeuGluThrThrAlaMetThrLeuPheProValLeuLeuPheLeu 23
           ||||||      |||||||:::           |||:::   :::   |||   |||
Db      82 CATCCTTCCATGGCTCTGAAGAATAAATTCAGTTGTTTATGGATCTTGGGTCTGTGTTTG 141

Qy      24 ValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAlaPheThrAla 43
           ||||||                |||:::          ||||||   |||
Db     142 GTAGCCACTACATCTTCCAAAATCCCATCC------ATCACTGACCCACACTTTATA--- 192

Qy      44 LeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArg 63
                                          :::      |||||||||   |||
Db     193 --------------------------GACAACTGCATAGAAGCCCACAACGAATGGCGT 225

Qy      64 ArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAla 83
             |||:::|||||||||  :::|||      |||   |||:::|||      |||
Db     226 GGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACATGATTTGGGATAAAGGTTTAGCA 285

Qy      84 AlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArg 103
             |||:::   ||||||||||||||   :::   |||::::::      |||:::
Db     286 AAGATGGCTAAAGCATGGGCAAACCAGTGCAAATTTGAACATAATGACTGTTTGGATAAA 345

Qy     104 MetThrSerLeuLysCys--------------------GlyGluAsnLeuTyrMetSer 116
             |||   ||||||                        |||||||||:::::::::
Db     346 ------TCATATAAATGCTATGCAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGT 399

Qy     117 SerAlaProSer---SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAsp 135
                 |||   :::        ||||||   :::|||:::::|||
Db     400 GGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGGTATAATGAAACCCAATTT 459

Qy     136 PheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnVal 155
           :::||||||                :::   :::   |||   |||||||||||||||:::
Db     460 TATGATTTT------GATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACAGTTA 513

Qy     156 ValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn---GlnLys 174
           ||||||   :::|||:::   |||||||||      |||   |||||||||
Db     514 GTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTTGGGGGA 573

Qy     175 ValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeu 194
                    :::||||||   |||   ||||||||||||:::||||||
```

```
Db    574 GCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAAT------ 627

Qy    195 TyrValProTyrGluGlnGlyAlaProCysAlaSerCys------ProAspAsnCysAsp 212
Db    628 ATGCCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTA 687

Qy    213 AspGlyLeuCys 216
Db    688 AAGAACCTCTGC 699
```

RESULT 13
US-10-137-865-261
; Sequence 261, Application US/10137865
; Publication No. US20030032155A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 261
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-865-261

Alignment Scores:

Pred. No.:	1.74e-26	Length:	882
Score:	305.50	Matches:	80
Percent Similarity:	49.55%	Conservative:	31
Best Local Similarity:	35.71%	Mismatches:	82
Query Match:	21.27%	Indels:	31
DB:	9	Gaps:	10

US-09-698-781-3 (1-258) x US-10-137-865-261 (1-882)

```
Qy      6 HisPro------AlaLeuGluThrThrAlaMetThrLeuProValLeuLeuPheLeu 23
Db     82 CATCCTTCCATGGCTCTGAAGAATAAATTCAGTTGTTTATGGATCTTGGGTCTGTGTTTG 141

Qy     24 ValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAlaPheThrAla 43
Db    142 GTAGCCACTACATCTTCCAAAATCCCATCC------ATCACTGACCCACACTTTATA--- 192

Qy     44 LeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArg 63
Db    193 -------------------------GACAACTGCATAGAAGCCCACAACGAATGGCGT 225

Qy     64 ArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAla 83
Db    226 GGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACATGATTTGGGATAAAGGTTTAGCA 285

Qy     84 AlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArg 103
```

```
Db    286 AAGATGGCTAAAGCATGGGCAAACCAGTGCAAATTTGAACATAATGACTGTTTGGATAAA 345

Qy    104 MetThrSerLeuLysCys--------------------GlyGluAsnLeuTyrMetSer 116
Db    346 ------TCATATAAATGCTATGCAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGT 399

Qy    117 SerAlaProSer---SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAsp 135
Db    400 GGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGGTATAATGAAACCCAATTT 459

Qy    136 PheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnVal 155
Db    460 TATGATTTT------GATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACAGTTA 513

Qy    156 ValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn---GlnLys 174
Db    514 GTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTTGGGGGA 573

Qy    175 ValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeu 194
Db    574 GCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAAT------ 627

Qy    195 TyrValProTyrGluGlnGlyAlaProCysAlaSerCys------ProAspAsnCysAsp 212
Db    628 ATGCCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTA 687

Qy    213 AspGlyLeuCys 216
Db    688 AAGAACCTCTGC 699
```

RESULT 14
US-10-140-474-261
; Sequence 261, Application US/10140474
; Publication No. US20030032156A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C162
; CURRENT APPLICATION NUMBER: US/10/140,474
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 261
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-474-261

Alignment Scores:

Pred. No.:	1.74e-26	Length:	882
Score:	305.50	Matches:	80
Percent Similarity:	49.55%	Conservative:	31
Best Local Similarity:	35.71%	Mismatches:	82
Query Match:	21.27%	Indels:	31
DB:	9	Gaps:	10

```
US-09-698-781-3 (1-258) x US-10-140-474-261 (1-882)

Qy       6 HisPro------AlaLeuGluThrThrAlaMetThrLeuPheProValLeuLeuPheLeu 23
Db      82 CATCCTTCCATGGCTCTGAAGAATAAATTCAGTTGTTTATGGATCTTGGGTCTGTGTTTG 141

Qy      24 ValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAlaPheThrAla 43
Db     142 GTAGCCACTACATCTTCCAAAATCCCATCC------ATCACTGACCCACACTTTATA--- 192

Qy      44 LeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArg 63
Db     193 --------------------------GACAACTGCATAGAAGCCCACAACGAATGGCGT 225

Qy      64 ArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAla 83
Db     226 GGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACATGATTTGGGATAAAGGTTTAGCA 285

Qy      84 AlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArg 103
Db     286 AAGATGGCTAAAGCATGGGCAAACCAGTGCAAATTTGAACATAATGACTGTTTGGATAAA 345

Qy     104 MetThrSerLeuLysCys--------------------GlyGluAsnLeuTyrMetSer 116
Db     346 ------TCATATAAATGCTATGCAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGT 399

Qy     117 SerAlaProSer---SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAsp 135
Db     400 GGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGGTATAATGAAACCCAATTT 459

Qy     136 PheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnVal 155
Db     460 TATGATTTT------GATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACAGTTA 513

Qy     156 ValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn---GlnLys 174
Db     514 GTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTTGGGGGA 573

Qy     175 ValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeu 194
Db     574 GCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAAT------ 627

Qy     195 TyrValProTyrGluGlnGlyAlaProCysAlaSerCys------ProAspAsnCysAsp 212
Db     628 ATGCCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTA 687

Qy     213 AspGlyLeuCys 216
Db     688 AAGAACCTCTGC 699

RESULT 15
US-10-142-431-261
; Sequence 261, Application US/10142431
; Publication No. US20030036179A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C251
;  CURRENT APPLICATION NUMBER: US/10/142,431
;  CURRENT FILING DATE:  2002-05-10
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 261
;   LENGTH: 882
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-142-431-261

Alignment Scores:
Pred. No.:                1.74e-26        Length:          882
Score:                    305.50          Matches:         80
Percent Similarity:       49.55%          Conservative:    31
Best Local Similarity:    35.71%          Mismatches:      82
Query Match:              21.27%          Indels:          31
DB:                       9               Gaps:            10

US-09-698-781-3 (1-258) x US-10-142-431-261 (1-882)

Qy       6 HisPro------AlaLeuGluThrThrAlaMetThrLeuPheProValLeuLeuPheLeu 23
Db      82 CATCCTTCCATGGCTCTGAAGAATAAATTCAGTTGTTTATGGATCTTGGGTCTGTGTTTG 141

Qy      24 ValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAlaPheThrAla 43
Db     142 GTAGCCACTACATCTTCCAAAATCCCATCC------ATCACTGACCCACACTTTATA--- 192

Qy      44 LeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsnGluLeuArg 63
Db     193 --------------------------GACAACTGCATAGAAGCCCACAACGAATGGCGT 225

Qy      64 ArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAla 83
Db     226 GGCAAAGTCAACCCTCCCGCGGCCGACATGAAATACATGATTTGGGATAAAGGTTTAGCA 285

Qy      84 AlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnProLysAspArg 103
Db     286 AAGATGGCTAAAGCATGGGCAAACCAGTGCAAATTTGAACATAATGACTGTTTGGATAAA 345

Qy     104 MetThrSerLeuLysCys--------------------GlyGluAsnLeuTyrMetSer 116
Db     346 ------TCATATAAATGCTATGCAGCTTTTGAATATGTTGGAGAAAATATCTGGTTAGGT 399

Qy     117 SerAlaProSer---SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAsp 135
Db     400 GGAATAAAGTCATTCACACCAAGACATGCCATTACGGCTTGGTATAATGAAACCCAATTT 459

Qy     136 PheAspPheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnVal 155
Db     460 TATGATTTT------GATAGTCTATCATGCTCCAGAGTCTGTGGCCATTATACACAGTTA 513

Qy     156 ValTrpTyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsn---GlnLys 174
Db     514 GTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTTGGGGGA 573

Qy     175 ValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeu 194
Db     574 GCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAAT------ 627

Qy     195 TyrValProTyrGluGlnGlyAlaProCysAlaSerCys------ProAspAsnCysAsp 212
Db     628 ATGCCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTA 687

Qy     213 AspGlyLeuCys 216
Db     688 AAGAACCTCTGC 699


Search completed: March 14, 2003, 05:30:18
Job time : 230.079 secs
```